

B1
const.

improves the yield of the secondary metabolite, provided however, that when the secondary metabolite is isopenicillin N, then the modulation is not mediated by transcription factor CPC1; when the secondary metabolite is sterigmatocystin, then the modulation is not through AflR, FadA, or FluG; when the secondary metabolite is aflatoxin, then the modulation is not through AflR; when the secondary metabolite is penicillin and the fungus is *Aspergillus nidulans*, then the modulation is not through mutations that result in expression of truncated forms of PacC or constitutively active forms of FadA; when the secondary metabolite is lovastatin and the fungus is *Aspergillus terreus*, then the modulation is not through expression of lovE; and when the gene involved in regulation of secondary metabolite production is from *Saccharomyces cerevisiae*, then the modulation is not through decreased activity or expression of Hog1, Bem2, Rim15, Sfl1, Ira1, Ssd1, Srb11, Swi4, Tpk3 or through increased activity or expression of Afl1, Dhh1, Inv7, Inv8, Ste21, Pet9, Mep2, Inv1, Inv5, Inv6, Inv9, Inv10, Inv11, Inv12, Inv13, Inv14, Inv15, Cdc25, Mcm1, Mga1, Phd2, Pho23, Ptc1, Rim1, Stp22, Tpk2 or Ypr1.

Please amend claim 15 to read as follows.

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15. (Amended) A method for improving production of a secondary metabolite by a fungus by increasing productivity of the secondary metabolite in the fungus, the method comprising modulating the expression of a gene involved in regulation of secondary metabolite production in a manner that improves the productivity of the secondary metabolite, provided however, that when the secondary metabolite is isopenicillin N, then the modulation is not mediated by transcription factor CPC1; when the secondary metabolite is sterigmatocystin, then the modulation is not through AflR, FadA, or FluG; when the secondary metabolite is aflatoxin, then the modulation is not through AflR; when the secondary metabolite is

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CON 4.

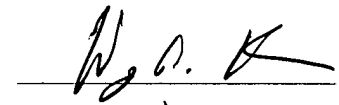
penicillin and the fungus is *Aspergillus nidulans*, then the modulation is not through mutations that result in expression of truncated forms of PacC or constitutively active forms of FadA, when the secondary metabolite is lovastatin and the fungus is *Aspergillus terreus*, then the modulation is not through expression of lovE; and when the gene involved in regulation of secondary metabolite production is from *Saccharomyces cerevisiae*, then the modulation is not through decreased activity or expression of Hog1, Bem2, Rim15, Sfl1, Ira1, Ssd1, Srb11, Swi4, Tpk3 or through increased activity or expression of Afl1, Dhh1, Inv7, Inv8, Ste21, Pet9, Mep2, Inv1, Inv5, Inv6, Inv9, Inv10, Inv11, Inv12, Inv13, Inv14, Inv15, Cdc25, Mcm1, Mga1, Phd2, Pho23, Ptc1, Rim1, Stp22, Tpk2 or Ypr1.

Claims 1 and 15 have been amended to specify that when the secondary metabolite is lovastatin and the fungus is *Aspergillus terreus*, then the modulation is not through expression of lovE. Support for lovE is found in Table 1 of the specification. This amendment is being made to exclude the teachings of WO 00/37629, which was included in the Information Disclosure Statement dated 21 June 2001. Although this reference is not prior art, it could potentially become prior art under 35 U.S.C. §102(e) if its counterpart U.S. application, Serial No.09/215,694 issues as a United States Patent.

A marked-up copy of the amended claims is shown in Exhibit A.

If the Examiner believes that any discussion of this reply would be helpful, the Examiner is invited to call the undersigned attorney by telephone at 781-938-1805.

Respectfully submitted,

A handwritten signature in black ink, appearing to read 'W. A. Keown', written over a horizontal line.

Wayne A. Keown, Ph.D.

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